

**REMARKS**

Reconsideration is requested.

Claims 10, 11 and 13-20, defining non-elected subject matter, have been canceled above, to advance prosecution.

Claims 1-9, 12 and 21 are pending.

The specification has been revised to delete embedded hyperlinks and other forms of browser-executable code. The specification has been revised to capitalize the term indicated as being a Trademark and provide a generic description of the same. Withdrawal of the objections to the specification stated on page 3 of the Office Action dated September 21, 2007 is requested.

The claims have been amended, without prejudice, to advance prosecution. Support for the claim revisions is believed to exist in the originally-filed application. Specifically, for example, basis for the revision to claim 1 with regard to the identity of the protein may be found in the unamended claim 1 as well as on page 2, line 14-18: page 3, lines 5-6, page 4, line 33 to page 5, line 3; page 26, lines 14-15; page 6, lines 35-37 and on page 30. line 15 to page 33, line 6. The claims have also been revised to refer to control plants, as opposed to wild type plants, as described, for example, on page 15, line 16; page 32, line 5 and page 33, lines 23-24 of the specification. No new matter has been added. Claim 21 has been added to define further

The Section 112, second paragraph, rejection of claims 1-9 and 12 is believed to be obviated by the above amendments. For completeness, the applicants note that TOB3 was a known term at the time of filing (see attached printouts of AF34078 (human TOB3) and AAK38648 (mouse TOB3). Moreover, it was also known that T0B3 belongs

to the AAA-ATPase family (see attached GenBank entry AF343078). Reconsideration and withdrawal of the rejection are requested.

To the extent not obviated by the above amendments, the Section 112, first paragraph "written description", rejection of claims "1, 2, 4 and 7-19" is traversed. (The Examiner perhaps intended to only reject claims 1, 2, 4 and 7-9 however clarification is requested if otherwise.) Reconsideration and withdrawal of the rejection are requested in view of the above and the following further comments.

The description on page 3, lines 5-6, discloses that the TAD protein comprises an ATPase domain. Moreover, on page 4, line 33 to page 5, line 4, it is disclosed that the homologues have in increasing order of preference at least 70%. 80%. 85%, 90%, 95% 96%, 97%. 98% or 99% sequence identity. An alternative definition (page 5, lines 6-9) states that the homologues have ATP binding and/or ATPase activity, and comprise a sequence of 22 consecutive amino acids having at least 90% sequence identity to a corresponding sequence in SEQ ID NO:2. The homologues of a TAD protein also encompass sequences that hybridize under stringent conditions to SEQ ID NO:1 (page 7, line 10-12). Stringent hybridization conditions are defined, for example, on page 8, line 10 to 31. Moreover, the applicants believe that a number of homologues to SEQ ID NO:2 are described on page 3, lines 20 to 23.

The claims are submitted to be supported by an adequate written description. Withdrawal of the Section 112, first paragraph, rejection of claims "1, 2, 4 and 7-19" is requested.

The Section 112, first paragraph "enablement", rejection of claims 1-9 and 12 is believed to be obviated by the above amendments. The claims are submitted to be

supported by an enabling disclosure. Many of the concerns raised by the Examiner in the rejection have been obviated by the above amendments and withdrawal of the Section 112, first paragraph "enablement", rejection of claims 1-9 and 12 is requested.

The Section 102 rejection of claims 1, 2 and 4-9 over Lorenzo (January, 2002, Plant Cell Physiology 43:27-34), is traversed. Reconsideration of the rejection are requested in view of the following distinguishing comments.

The applicants believe that the sequence of FsA1, disclosed by the cited art only has 22.8% sequence identity to SEQ ID NO:2 (that is when the corresponding sequences are compared, when the full length of FsA1 is compared with SEQ ID NO:2, then the sequence identity is less than 14%, see alignments attached as Annex 2).

The cited art is therefore not believed to anticipate the claimed invention which requires a minimum of 70% sequence identity to SEQ ID NO:2.

Withdrawal of the Section 102 rejection is requested.

The Section 102 rejection of claims 1-3, 8, 9 and 12 over Kwart (U.S. Patent Application Publication No. 2004/0168214), is traversed. Reconsideration and withdrawal of the rejection are requested in view of the attached alignment (see Annex 3) between SEQ ID NO:2 and the PHA2 protein sequence. Moreover, the cited reference is believed to be related to increased biomass, as opposed to see yield, as presently claimed.

Withdrawal of the Section 102 rejection is requested.

The claims are submitted to be in condition for allowance and a Notice to that effect is requested. The Examiner is requested to contact the undersigned in the event anything further is required in this regard.

HATZFELD et al.  
Appl. No. 10/551,228  
December 21, 2007  
Amendment

Respectfully submitted,

**NIXON & VANDERHYE P.C.**

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Facsimile: (703) 816-4100

## Annex 1: AF34078 (human TOB3) and AAK38648 (mouse TOB3)

ID AF34078 standard; RNA; HUM; 1966 BP.  
XX  
AC AF34078;  
XX  
SV AF34078.1  
XX  
DT 26-APR-2001 (Rel. 67, Created)  
DT 26-APR-2001 (Rel. 67, Last updated, Version 1)  
XX  
DE Homo sapiens TOB3 mRNA, complete cds.  
XX  
KW  
XX  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XX  
RN [1]  
RP 1-1966  
RA Parng C., Piepenhagen P.A., Casanova J., Pillai S.;  
RT "TOB3 is a novel AAA-ATPase involved in protein secretion";  
RL Unpublished.  
XX  
RN [2]  
RP 1-1966  
RA Parng C., Piepenhagen P.A., Casanova J., Pillai S.;  
RT  
RL Submitted (26-JAN-2001) to the EMBL/GenBank/DBJ databases.  
RL The MGH Cancer Center, Massachusetts General Hospital, Building 149, 13th  
RL St., Charlestown, MA 02129, USA  
XX  
DR ENSEMBL1; ENSG00000160072; ENST00000308647.  
DR GOA; Q96T67; Q96T67.  
DR SPTREMBL; Q96T67; Q96T67.  
XX  
FH Key Location/Qualifiers  
FH  
FT source 1..1966  
FT /chromosome="1"  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /dev\_stage="embryo day 16"  
FT CDS 67..1803  
FT /codon\_start=1  
FT /db\_xref="GOA:Q96T67"  
FT /db\_xref="SPTREMBL:Q96T67"  
FT /note="member of AAA-ATPase family"  
FT /product="TOB3"  
FT /protein\_id="AAK38647.1"  
FT /translation="MSWLFGIKGPKEGAGPPPPPLPPAQPGAEGGGDRGLGDRPAPKDK  
WSNFDPTCLERAAKAAARELEHCRYAKDALNLQMGEQTLQLEQQSKLKEYEAAVEQLKS  
EQIRAOAEERRKTLSESTRQHQARAQYQDKLAKRYEDQLKQQQLNEENLRKOEESVQ  
KOEAMRRATVERRMELRHKNEMLRVFAFAKAKAKAERENADIIREQIRLKASEHRQTVL  
ESIKTAGTLKGEGRFAFVTDWDKVTATVAGLTLAVCVYSAKNATLVAGRFIEARLGKP  
SIWRETSRTIVLEALRHDTQVSRSLSRPQDALEGVVLSPSLEARVRDIAIATLNTKKN  
RSLPRNILMYGDPDCKTLFAKKLPLUGGMDYAIMTGGDVAPMGGKGVMTAMHKLFDWAN  
TSRRGLLLFMDEADAFLRKRATEEISKDLKATLNAFLYHMGQHSNKFMLVLASNLPEQF  
DCAINSRIQVMVHFQDLPOQKEREPWVRLHFDNCVLKPATEGKQRLKLAQFDYGRKCSV  
ARLIECMSGREIAQIAVSWQATAYAGEDGVLTEAMMDTRVQDAVQQHQQKMCWLKAEC  
LC"  
XX  
SO Sequence 1966 BP; 410 A; 569 C; 683 G; 291 T; 5 other;  
ccagccgcgc gcgagtcaga ctcqqqtgqq ggtcccgccg gcggtagcgg cggcgccggt 60  
gcgagcatgt cgtggctcct cqqcctcagg ggcctcaagg gtgaaggcgc ggggcccgcg 120

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ccgccctttgc cggcccgccga gcccgggggg gggggcgggg gggaccggg gttgggagac 180
cggcccgccgc cccgggacaa atggggcaac ttccgaccca ccggcccgga ggcggccgcc 240
aaggcggggc gggagctgga gcctctcggt tatgccagg acgcccctga tctggcacag 300
atgcaggagc agacgctgca gttggagcaa cagtcacaag ccaagagga ttgggcccgc 360
gtggagcagc hcaagagaga gacagtcagg ggcagagctg agggagggag gaagaccctg 420
agggagggga cggggcgga ccaggccagg gcccatgacc aagacaagct ggcggcgccg 480
cgctacggg accaactgaa gcagcagcaa cctctcaatg aggagaattt acggagggag 540
gaggagctcg tgcagaagca ggaagccatg cggcgagcca cgtggagcg gaggatggag 600
ctggggccca agaatgagat gctgcgagtg gaggcgagg ccggggcgcg cgcgaaggcc 660
gagcgggaga atgcagacat catccggcag cagatccggc tgaaggcgtc cgaagaccgt 720
cagaacgtct tggagtcac caggacggct ggcacctgtt ttggggaaag atctcgtgcc 780
tttgtgacag actgggacaa agtgacagcc aggtcgctg cctggcgtgt 840
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gggaagccgt cctcagtgag ggagacgttc cgcatacagg tggllgggg gctgcggcac 960
cccatccagg tcaacccggt cgtctcagc cgaacccagg acggctgga ggtgtgtgt 1020
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aagacccgca gctgttccg gaacattctg atgcacggg caccaggcc cgggagggag 1140
ctgtttgcca agaaacttcc cctgcactca ggcattgagc atgcacatc gacaggcggg 1200
gacgtggccc ccatgggggg gaaaggcggt acccactg ccaagctctt tgaactgggc 1260
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gagcgggagc cctgggctgag actgcatctt gacaactgtg tctttaagcc ggccacagaa 1560
ggaaagcagc gcttgaagct ggcacagttt gactacggga ggaagctct cagggtcgt 1620
cggctgacgg agggcatgtc gggccggggg atcgctcagc tggcgctgct cttggcaggg 1680
acggcgctac cgtccgagcg cggggtctct accgagccca tcatggacac ccgctgcca 1740
gagctgctcc agggagggg gcggaagatg tctgtgctga aggcgggaag atcgctgct 1800
tgagaggggg catgtaatgc cgggaagatg caccgctggt cgtgtctgg agggccacgg 1860
cgtatgntcc aaggacgggg tccctgacga ggcctgctg gacgctgct tgcgaagant 1920
ntccagcag caccagcaga tcatgctgt gctgaagggg gagagg 1966

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LOCUS      AF143079                1941 bp    mRNA    linear    ROD 23-APR-2001
DEFINITION Mus musculus TOB3 mRNA, complete cds.
ACCESSION  AF143079
VERSION    AF143079.1  GI:13752412
KEYWORDS   .
SOURCE     Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1941)
AUTHORS   Farnig,C., Piepenhagen,P.A., Casanova,J. and Pillai,S.
TITLE     TOB3 is a novel AAA-ATPase involved in protein secretion
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 1941)
AUTHORS   Farnig,C., Piepenhagen,P.A., Casanova,J. and Pillai,S.
TITLE     Direct Submission
JOURNAL   Submitted (26-JAN-2001) The MCH Cancer Center, Massachusetts
            General Hospital, Building 149, 13th St., Charlestown, MA 02129,
            USA

FEATURES             Location/Qualifiers
     source           1..1941
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
     CDS              142..1917
                     /note="member of AAA-ATPase family"
                     /codon_start=1
                     /product="TOB3"
                     /protein_id="AAK38648.1"
                     /db_xref="GI:13752413"
                     /translation="MSWLPGIKCKKCEGTGPPLPLPPAQPGEAGGGGDRGAGDRPSPKD
            KWSNFDPTGLERAAKAARELEHSRIIAKEALSLAQMQRQTLDLEQQSKLKEYEAAVEQL
            KSEQIRVQAEERRKLTLEETROHQARAQYODKLARQRYEDQLKCOOLLNEENLRKQEE

```

SVQKQEAIRRATVEREMELRHKNEMLRVEAEARARAKADRENADIIRFQIRLKAAEHR  
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 RLGKPSLVRETSKISVLEALRHPTQVSRRLVSRPDALGVILSPSLEARVRDIAIAT  
 RNTKKNKSLYRNVLMYCDEGTGKTIIPAKKLALHSGMDYAIMTGGDVAPMGREGVTAMH  
 KVFDWASTSRRCLLLFVDEADAFLRKRATEKISEDLRATINAFLEHRTUQHSSKFMLVL  
 ASNQPEOPDWAINDRIDEMVCFALPQREERERLVRMYFDKYVLKPATECKQRLLKVAQF  
 DYGKKCSEVAQLTERMSGREIAQLAVAWQAMAYSSEDGVLTEAMMDARVQDAVQGHQO  
 KMQLKVRPDSQTNKPPHDSLLSC"

## ORIGIN

```

1  Enattagagc ctgnactncc tactaaatgc cccnctngat tgcallctggc aaacccacccc
61  cgtttctgggn cgtgggtggg ctgcnaggag cctcggcagc caagccccgg acgggtccgcc
121  gagggcgggg agttgcagac catgtctgg ctcttcggca tcaaggggccc caaggggcgu
181  ggccacagggc ctccgcctgcc cttagccggc gctcaacccg gggcgggggg cggcgggtgac
241  cgcggggggc gagaccggcc atcgccnag gacaaatgga gccacttcga cccgacgggc
301  ctgggaacgtg cggcccaagg cgtctcgag ctggagcact cgcgcctatg caaggaggca
361  ctgagtctcg cacagatgca ggagcagacg ctgcagctgg aacagcctac caagctcaag
421  gagtacgaag ctgcccgtaga gtagctgaag aqcgaaacga tccgtctgca agccgaggaa
481  agaaggaaaa cccctgactga agagacacga cagcccccgg ctaggggccc gtaaccggat
541  aagctcgctc gacagcctga tyaggaccag ctgaaccac agcaactctc gaatgaagag
601  aacttaagga aacaaaggga gtctgtgca agcaggagg ccaacgggg agccactctg
661  gagcgcgagc tggagctgag gcataaaaa gngctgttgc ggggtggaagc tgaagcccg
721  gcacggggcc aagctgctga agagaaagca gatatcatc gggaaacagat tgcactcag
781  qctgctgagc acgcgcagac catcttggag tctatcagga cagctggcac ctgtctggg
841  gaaggtttcc gtgcatttgc gacagactgg gacaaagtga cgtctacggg ggtctgggtg
901  accctattag ctgttggagt ctactctgca aagaatgcta ctctgttgc cggctgggtat
961  attgaggccc gattgggaaa gccgctcttg gtgagagaga cctcccgaa cctcgtgcta
1021  gaggcattga ggcactccat ccaggtcagc aggcgactgg tcagcaqacc ccgggatgca
1081  ttggagggcg tcatcctcag ccttagcctg qaqqnaccgg tccgagatat tggcatcga
1141  acaagaaata ccaagaagaa caaaagcctg tataggaagc tctctgatga tgggcccccg
1201  gggactggca agacactatc tgcgaagaaa cttgcaactg attcaggaat ggaactacgc
1261  atcatgacag gcyggggcgt ggccccaatg gggcgggagg ctgtgactgc catgcacaag
1321  gctctcgact gggcaagcac caqccgacga ggcctccgc tcttctgga tgaagcagac
1381  gccttcccca ggaaacgagc qactgnaagc ataagctgaag acctcagggc tactctgaat
1441  gcttctctac acaggacagg acgucacagt agtaagtcca tgcctggctc ggccagtaac
1501  cngcttgagc agtttgaact ggctatcaat gaccgacttg acagatggc ctgctttgcc
1561  ctgccacagc gggaggagcg agagcgctcg gtgagaatgc attttgacaa gtatgctctt
1621  aagccggcca cagaaggaaa gcaagccttg aaggtggccc agtttgacta tggaaagaaa
1681  tgcacagagg ttgcacagct aagggggggg atgacaggcc gggagatttc tngcttgc
1741  gtggcgtggc aggcacatggc ctattcatct gaggatggag tctcagcga agctatgatg
1801  gatgcctgtg tgcaggatgc tgtgcagcag caccagcaga agatgcagtg gcttaaaqta
1861  gagagacccg atctccagac caacaaagcgc ccactcctt cactcctcag ctgctngct
1921  ggaactggac accttgcaca c

```

//

## Annex 2: alignment of SEQ ID NO: 2 with FsA1 (full length and ATPase domain)

```
#####
# Program: needle
# Rundate: Mon Dec 10 11:10:08 2007
# Align_format: srspair
# Report_file: outfile
#####
#=====
```

```
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: FsA1
# Matrix: BLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
```

```
#
# Length: 470
# Identity: 63/470 (13.4%)
# Similarity: 108/470 (23.0%)
# Gaps: 274/470 (58.3%)
# Score: 158.0
#
#
#=====
```

```
SEQIDNO2      1                                     0
FsA1           1 MALETKHPRVPADETCSAKCSKOCGLKQYYLQIIHHDHQLQVRQKTHNL 50
SEQIDNO2      1                                     0
FsA1           51 NRLEAQRNEFNSRVRMLREELQLLQEPGSYVGEVVKVMGKNKVLVKVHSE 100
SEQIDNO2      1                                     0
FsA1          101 GKYVVDIDKNIDITKTFSTRVALRNDGYVLHLILPSKVDPLVNLMKVEK 150
SEQIDNO2      1                                     MLFYGP 6
FsA1          151 VPDSTYDMIGGLDQOIKEIKEVIELPIKIPELFLESLGIAQPKGVLLYCP 200
SEQIDNO2      7 PGTGKTMVAREIARKSGLDYAMMTGGD-VAPLCAQAVTKIIEIFDWAKKS 55
FsA1          201 PGTGSKILLARAVAHHTDCTFIRVGGSELVOKYIGEGSRMVRELFVMARE 249
SEQIDNO2      56 NKGLLLFIDEADAFLECR----NSTYMSEAQRSAINALLFRTGDOS-RDV 100
FsA1          250 HAPSIIFMDFTDSIGSARMESGGSGNGDSEVQDHMLELLNQLOGFESIKQT 299
SEQIDNO2      101 VLVLATNRPGDLDSAV--TDKIDEVIEFPLPQRFERFKLLKLY -LN-- 143
FsA1          300 KVLMTNRITDILDQALLRPCRIDRKIEFPNPNRESRFIDILKHSRRMNL 349
SEQIDNO2      144 -----KYLAGEGDSDSNSKW-----GHLFKKNQQR---ITIODLSDDV 179
FsA1          350 RGIDLKKIAEKMNGASGAELKAVCTEAGMFALTAERRVKLVIQEDFRMAV 399
SEQIDNO2      180 IREAAKKIE-GPSGREIAKLMAVQATVYGSPDCVLDSQLPKKEIVDYKVA 228
FsA1          400 AKVMKKETEKMSLRKLWK 418
SEQIDNO2      229 EHHQRIKLAAFGMEPTYQGN 248
FsA1          419 418
#-----
```



```
#-----
#####
# Program: needle
# RunDate: Mon Dec 10 11:14:31 2007
# Align_format: arspair
# Report_file: outfile
#####
#=====
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: FsAlpart
# Matrix: EBLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
#
# Length: 276
# Identity:      63/276 (22.8%)
# Similarity:    109/276 (39.1%)
# Gaps:          80/276 (29.0%)
# Score: 158.0
#
#
#=====
SEQIDNO2      1 MLFYCDPCTGKTMVAREIARKSGLDYAMMTGGD-VAPLGAQAVTKIHEIF      49
               :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
FsAlpart      1 VLLYGPGGTGKTLARAVAHHTDCTFIRVSGSELVOKYIGEGSRMVRELF      50
SEQIDNO2     50 DWAKKSNKGLLLFIDEADAFLCER---NSTYMSEAQRSAINALLFRTGD      95
               :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
FsAlpart     51 VMARE-HAPSIIFMDRIIDISIGSARMESGSGNGDSEVQDHMLELLNQLDGF      99
SEQIDNO2     96 QS-RDVVLVLATNRPGLDSAV--TDRIDEVIEFPPIQEERFKLLKLY-     141
               :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
FsAlpart    100 ESIKQIKVIMRTNRIDILDQALLRPGRIDRKIEFPNPNRESRFDJIKIHS     149
SEQIDNO2    142 LN-----KYLAGEGSDSDSNKW-----GHLFKKNQQKR---ITIO     173
               :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
FsAlpart    150 RRMNIMRGIDLKKIAEKMNQASCAELKAVCTAGMPALTAERRVRKLVITQE     199
SEQIDNO2    174 DLSDDVIREAAKKIE-GFSGREIAKLMAVQATVYCSFDCVLDLSOLFKEI     222
               :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
FsAlpart    200 DFEMAVAKVMKKETKNTMLRKLWK                                  224
SEQIDNO2    223 VDYKVAEHHQRIKLAAEGMEPTYQGN      248
FsAlpart    225                                  224
#
#-----
```

## Annex 3: alignment of SEQ ID NO: 2 with PHA2

```
#####
# Program: needle
# Run date: Mon Dec 10 11:16:34 2007
# Align_format: swpair
# Report_file: outfile
#####
```

```
=====
```

```
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: StPHA2
# Matrix: EBLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
#
# Length: 1160
# Identity:      8/1160 ( 0.7%)
# Similarity:    10/1160 ( 1.6%)
# Gaps:          1120/1160 (96.6%)
# Score: 20.0
#
#
```

```
#####
```

SEQIDNO2	1	MLPYGPPGTGKTMVAREIARKSGLDYAMMTGGDVAPLGAAVTKIHSIFD	50
StPHA2	1		0
SEQIDNO2	51	WAKKSNKGLLLFIDEADAFICERNSTYMSEAORSALNALLFRITGDQSRDV	100
StPHA2	1		0
SEQIDNO2	101	VLVLAINRPGDLDASVTDRIDEVIEFPLQEDERFKLLKLYLNKYLAGEG	150
StPHA2	1		0
SEQIDNO2	151	DSDSNSIKWGHLEKKNQOKRITIQDLSDDVTREAAKKIEGFSGREIAKLMA	200
StPHA2	1		0
SEQIDNO2	201	SVQATVYGSPDCVLDSQLFKRIVDYK---VAEHIIQRIKLAAEGMEPTYQG	247
StPHA2	1	MAKATISLEETIKNETVDLEKIPTREVFQQLKCSREGLTSDEGA	12
SEQIDNO2	240	N	240
StPHA2	13	NRLQIFCPNKLSEKKESKILKFLGFMWNPLSWVMEAAAIMAIALANGNGK	92
SEQIDNO2	249		240
StPHA2	93	PPDWQDFVGIVCLLVINSTISFIEENNAGNAAAAIMAGLAPKTKVLRDGR	142
SEQIDNO2	249		248
StPHA2	143	WSEQRAMILVPCDIISVKLGDIVPADARLLEGDPLKIDOSALTGESLPVT	192
SEQIDNO2	249		240
StPHA2	193	KNPGDEVFSGSTCKOCELEAVVIATGVHTFEGKAHLVDSTNNVGHIFQKV	212
SEQIDNO2	249		248
StPHA2	243	LTAIGNFCICSIAGVMLEIIVMYTIQHRKYRDGIDNLLVLLIGGIPAM	292
SEQIDNO2	249		248

StPHA2	293	PTVLSVTMATGSHRTSQQGAITKRMTAIEEMAGMDVLCSDKIGTLTLNKL	342
SEQIDNO2	249		248
StPHA2	343	SVDKTLVEVFVKCVDKEYVLLPARASRVENQDAIDACMVGMADIKEAR	392
SEQIDNO2	249		248
StPHA2	393	AGIREVHFLLPNNPVDKRTALTYIDNNGNWHRASGAPEQILDLCNCKEDV	442
SEQIDNO2	249		248
StPHA2	443	RRKVHSMIDKYAEAGLRSLAVARQEVPEKSKESACCFWOFVGLLPLEDFP	492
SEQIDNO2	249		240
StPHA2	493	RHDSAETIRRALNLGVNVKMITGQQALAIKETCRRRLGMGTNMYPSASLLG	542
SEQIDNO2	249		248
StPHA2	543	ODKSSIASLPVEELIEKADGFAGVFPEIKYEIVKKLQERKHIVGMTGDC	592
SEQIDNO2	249		240
StPHA2	593	VNDAPALKKADIGIAVADATDAARGASPIVLTEPCLSVIIISAVLTSRAIF	642
SEQIDNO2	249		248
StPHA2	643	QRMKNYTIYAVSITIRIVGFEMLIALIWKYDFSAFMVLTIAILNDGTIMT	692
SEQIDNO2	249		248
StPHA2	693	ISKDRVKPSFMPDSWKLNEIFATGVVLGGYOALMTVLFFWAMHDYKFFSD	742
SEQIDNO2	249		248
StPHA2	743	KFGVKDIRESDREEMMSALYLQVSIISOALIFVTRSRWSFVRPGLLMI	792
SEQIDNO2	249		248
StPHA2	793	AFLIAQLVATLIAVYADWTFARVKGCCWOWAGVIWIFSIIVTYFPLDIMKF	842
SEQIDNO2	249		248
StPHA2	843	AIRYILSGKAWNNLIDNKTAFTTKIDYGKEEREQAQWALAQRTIHGLOPPE	892
SEQIDNO2	249		248
StPHA2	893	ASNLDFNEKNSYRELSFAEQAKRRAEMARLRELHNLKQGHVESVVKLGLD	942
SEQIDNO2	249	248	
StPHA2	943	IETIQQHYTV	952

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